RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/725, 019A_

Source: _____

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IFW16

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RAW SEQUENCE LISTING              DATE: 12/23/2004
PATENT APPLICATION:  US/09/725,019A    TIME: 14:34:23

Input Set :  N:\Crf3\RULE60\09725019a.raw.txt
Output Set:  N:\CRF4\12232004\I725019A.raw
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 1 <110> APPLICANT: Thompson, John E.
 2        Wang, Tzann-Wei
 3        Lu, Dongen Lilly
 4 <120> TITLE OF INVENTION: DNA ENCODING A PLANT DEOXYHYPUSINE SYNTHASE, TRANSGENIC
 5        PLANTS AND A METHOD FOR CONTROLLING PROGRAMMED CELL
 6        DEATH IN PLANTS
 7 <130> FILE REFERENCE: 10799/9
 8 <140> CURRENT APPLICATION NUMBER: US/09/725,019A
 9 <141> CURRENT FILING DATE: 2000-11-29
10 <150> PRIOR APPLICATION NUMBER: US/09/597,771
11 <151> PRIOR FILING DATE: 2000-06-19
12 <150> PRIOR APPLICATION NUMBER: 09/348,675
13 <151> PRIOR FILING DATE: 1999-07-06
14 <160> NUMBER OF SEQ ID NOS: 35
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1609
19 <212> TYPE: DNA
20 <213> ORGANISM: Lycopersicon sp.
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (54..1196)
24 <220> FEATURE:
25 <223> OTHER INFORMATION: DHS
26 <400> SEQUENCE: 1
27        cgcagaaact cgcggcggca gtcttgttcc ctacataatc ttggtctgca ata atg      56
28                                                                     Met
29                                                                      1
30        gga gaa gct ctg aag tac agt atc atg gac tca gta aga tcg gta gtt    104
31        Gly Glu Ala Leu Lys Tyr Ser Ile Met Asp Ser Val Arg Ser Val Val
32                        5                  10                  15
33        ttc aaa gaa tcc gaa aat cta gaa ggt tct tgc act aaa atc gag ggc    152
34        Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu Gly
35                   20                  25                  30
36        tac gac ttc aat aaa ggc gtt aac tat gct gag ctg atc aag tcc atg    200
37        Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser Met
38              35                  40                  45
39        gtt tcc act ggt ttc caa gca tct aat ctt ggt gac gcc att gca att    248
40        Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala Ile
41         50                  55                  60                  65
42        gtt aat caa atg cta gat tgg agg ctt tca cat gag ctg ccc acg gag    296
43        Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr Glu
44                        70                  75                  80
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45      gat tgc agt gaa gaa gaa aga gat gtt gca tac aga gag tcg gta acc      344
46      Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val Thr
47              85                      90                  95
48      tgc aaa atc ttc ttg ggg ttc act tca aac ctt gtt tct tct ggt gtt      392
49      Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val
50              100                     105                 110
51      aga gac act gtc cgc tac ctt gtt cag cac cgg atg gtt gat gtt gtg      440
52      Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val Val
53              115                     120                 125
54      gtt act aca gct ggt ggt att gaa gag gat ctc ata aag tgc ctc gca      488
55      Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu Ala
56      130                     135                 140                 145
57      cca acc tac aag ggg gac ttc tct tta cct gga gct tct cta cga tcg      536
58      Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg Ser
59              150                     155                 160
60      aaa gga ttg aac cgt att ggt aac tta ttg gtt cct aat gac aac tac      584
61      Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr
62              165                     170                 175
63      tgc aaa ttt gag aat tgg atc atc cca gtt ttt gac caa atg tat gag      632
64      Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr Glu
65              180                     185                 190
66      gag cag att aat gag aag gtt cta tgg aca cca tct aaa gtc att gct      680
67      Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile Ala
68              195                     200                 205
69      cgt ctg ggt aaa gaa att aat gat gaa acc tca tac ttg tat tgg gct      728
70      Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp Ala
71      210                     215                 220                 225
72      tac aag aac cgg att cct gtc ttc tgt cct ggc ttg acg gat gga tca      776
73      Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser
74              230                     235                 240
75      ctt ggt gac atg cta tac ttc cat tct ttc aaa aag ggt gat cca gat      824
76      Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro Asp
77              245                     250                 255
78      aat cca gat ctt aat cct ggt cta gtc ata gac att gta gga gat att      872
79      Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp Ile
80              260                     265                 270
81      agg gcc atg aat ggt gaa gct gtc cat gct ggt ttg agg aag aca gga      920
82      Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr Gly
83              275                     280                 285
84      atg att ata ctg ggt gga ggg ctg cct aag cac cat gtt tgc aat gcc      968
85      Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Val Cys Asn Ala
86      290                     295                 300                 305
87      aat atg atg cgc aat ggt gca gat ttt gcc gtc ttc att aac acc gca      1016
88      Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr Ala
89              310                     315                 320
90      caa gag ttt gat ggt agt gac tct ggt gcc cgt cct gat gaa gct gta      1064
91      Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val
92              325                     330                 335
93      tca tgg gga aag ata cgt ggt ggt gcc aag act gtg aag gtg cat tgt      1112
```

```
94        Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His Cys
95                  340                 345                 350
96        gat gca acc att gca ttt ccc ata tta gta gct gag aca ttt gca gct        1160
97        Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala Ala
98                  355                 360                 365
99        aag agt aag gaa ttc tcc cag ata agg tgc caa gtt tgaacattga              1206
100       Lys Ser Lys Glu Phe Ser Gln Ile Arg Cys Gln Val
101       370                 375                 380
102       ggaagctgtc cttccgacca cacatatgaa ttgctagctt ttgaagccaa cttgctagtg       1266
103       tgcagcacca tttattctgc aaaactgact agagagcagg gtatattcct ctaccccgag       1326
104       ttagacgaca tcctgtatgg ttcaaattaa ttattttct ccccttcaca ccatgttatt        1386
105       tagttctctt cctcttcgaa agtgaagagc ttagatgttc ataggttttg aattatgttg       1446
106       gaggttggtg ataactgact agtcctctta ccatatagat aatgtatcct tgtactatga       1506
107       gattttgggt gtgtttgata ccaaggaaaa tgtttatttg gaaaacaatt ggattttaa        1566
108       tttatttttt cttgtttaaa aaaaaaaaaa aaaaaaaaaa aaa                         1609
110   <210> SEQ ID NO: 2
111   <211> LENGTH: 381
112   <212> TYPE: PRT
113   <213> ORGANISM: Lycopersicon sp.
114   <220> FEATURE:
115   <223> OTHER INFORMATION: DHS
116   <400> SEQUENCE: 2
117       Met Gly Glu Ala Leu Lys Tyr Ser Ile Met Asp Ser Val Arg Ser Val
118       1                   5                   10                  15
119       Val Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu
120                   20                  25                  30
121       Gly Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser
122                   35                  40                  45
123       Met Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala
124           50                  55                  60
125       Ile Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr
126       65                  70                  75                  80
127       Glu Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val
128                   85                  90                  95
129       Thr Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly
130                   100                 105                 110
131       Val Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val
132                   115                 120                 125
133       Val Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu
134           130                 135                 140
135       Ala Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg
136       145                 150                 155                 160
137       Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn
138                   165                 170                 175
139       Tyr Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr
140                   180                 185                 190
141       Glu Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile
142                   195                 200                 205
143       Ala Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp
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Input Set : N:\Crf3\RULE60\09725019a.raw.txt
Output Set: N:\CRF4\12232004\I725019A.raw

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144          210                  215                  220
145     Ala Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly
146     225                  230                  235                  240
147     Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro
148                     245                  250                  255
149     Asp Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp
150                     260                  265                  270
151     Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr
152                 275                  280                  285
153     Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Val Cys Asn
154         290                  295                  300
155     Ala Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr
156     305                  310                  315                  320
157     Ala Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala
158                     325                  330                  335
159     Val Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His
160                     340                  345                  350
161     Cys Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala
162                 355                  360                  365
163     Ala Lys Ser Lys Glu Phe Ser Gln Ile Arg Cys Gln Val
164         370                  375                  380
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 24
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
172 <400> SEQUENCE: 3
173     agtctagaag gtgctcgtcc tgat                                    24
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 34
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
181 <400> SEQUENCE: 4
182     gactgcagtc gacatcgatt tttttttttt tttt                         34
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 2272
186 <212> TYPE: DNA
187 <213> ORGANISM: Arabidopsis sp.
188 <220> FEATURE:
189 <221> NAME/KEY: CDS
190 <222> LOCATION: (68..265, 348..536, 624..842, 979..1065,
191     1154..1258, 1575..1862)
192 <400> SEQUENCE: 5
193     gaactcccaa aaccctctac tactacactt tcagatccaa ggaaatcaat tttgtcattc   60
194     gagcaac atg gag gat gat cgt gtt ttc tct tcg gtt cac tca aca gtt     109
195             Met Glu Asp Asp Arg Val Phe Ser Ser Val His Ser Thr Val
```

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196                 1               5                       10
197       ttc aaa gaa tcc gaa tca ttg gaa gga aag tgt gat aaa atc gaa gga   157
198       Phe Lys Glu Ser Glu Ser Leu Glu Gly Lys Cys Asp Lys Ile Glu Gly
199        15                  20                  25                  30
200       tac gat ttc aat caa gga gta gat tac cca aag ctt atg cga tcc atg   205
201       Tyr Asp Phe Asn Gln Gly Val Asp Tyr Pro Lys Leu Met Arg Ser Met
202                          35                  40                  45
203       ctc acc acc gga ttt caa gcc tcg aat ctc ggc gaa gct att gat gtc   253
204       Leu Thr Thr Gly Phe Gln Ala Ser Asn Leu Gly Glu Ala Ile Asp Val
205                      50                  55                  60
206       gtc aat caa atg gttcgtttct cgaattcatc aaaaataaaa attccttctt       305
207       Val Asn Gln Met
208                  65
209       tttgttttcc tttgttttgg gtgaattagt aatgacaaag ag ttt gaa ttt gta   359
210                                                         Phe Glu Phe Val
211                                                                       70
212       ttg aag cta gat tgg aga ctg gct gat gaa act aca gta gct gaa gac   407
213       Leu Lys Leu Asp Trp Arg Leu Ala Asp Glu Thr Thr Val Ala Glu Asp
214                      75                  80                  85
215       tgt agt gaa gag gag aag aat cca tcg ttt aga gag tct gtc aag tgt   455
216       Cys Ser Glu Glu Glu Lys Asn Pro Ser Phe Arg Glu Ser Val Lys Cys
217                      90                  95                  100
218       aaa atc ttt cta ggt ttc act tca aat ctt gtt tca tct ggt gtt aga   503
219       Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val Arg
220                  105                 110                 115
221       gat act att cgt tat ctt gtt cag cat cat atg gtttgtgatt tttgctttat   556
222       Asp Thr Ile Arg Tyr Leu Val Gln His His Met
223            120                 125
224       caccctgctt ttttatagat gttaaaattt tcgagcttta gttttgattt caatggtttt   616
225       tctgcag gtt gat gtt ata gtc acg aca act ggt ggt gtt gag gaa gat   665
226               Val Asp Val Ile Val Thr Thr Gly Gly Val Glu Glu Asp
227                130                 135                 140
228       ctc ata aaa tgc ctt gca cct aca ttt aaa ggt gat ttc tct cta cct   713
229       Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ser Leu Pro
230            145                 150                 155
231       gga gct tat tta agg tca aag gga ttg aac cga att ggg aat ttg ctg   761
232       Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu
233       160                 165                 170                 175
234       gtt cct aat gat aac tac tgc aag ttt gag gat tgg atc att ccc atc   809
235       Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile
236                      180                 185                 190
237       ttt gac gag atg ttg aag gaa cag aaa gaa gag gtattgcttt atctttcctt   862
238       Phe Asp Glu Met Leu Lys Glu Gln Lys Glu Glu
239                195                 200
240       tttatatgat ttgagatgat tctgtttgtg cgtcactagt ggagatagat tttgattcct   922
241       ctcttgcatc attgacttcg ttggtgaatc cttctttctc tggtttttcc ttgtag       978
242       aat gtg ttg tgg act cct tct aaa ctg tta gca cgg ctg gga aaa gaa   1026
243       Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys Glu
244                205                 210                 215
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/23/2004
PATENT APPLICATION: US/09/725,019A TIME: 14:34:24

Input Set : N:\Crf3\RULE60\09725019a.raw.txt
Output Set: N:\CRF4\12232004\I725019A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; N Pos. 6
Seq#:31; N Pos. 542

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VARIABLE LOCATION SUMMARY   DATE: 12/23/2004
PATENT APPLICATION: US/09/725,019A   TIME: 14:34:24

Input Set : N:\Crf3\RULE60\09725019a.raw.txt
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Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:19; N Pos. 6
Seq#:31; N Pos. 542

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/725,019A

DATE: 12/23/2004
TIME: 14:34:24

Input Set : **N:\Crf3\RULE60\09725019a.raw.txt**
Output Set: **N:\CRF4\12232004\I725019A.raw**

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L:764 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:19
L:764 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:19
L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:496
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